FIG.1

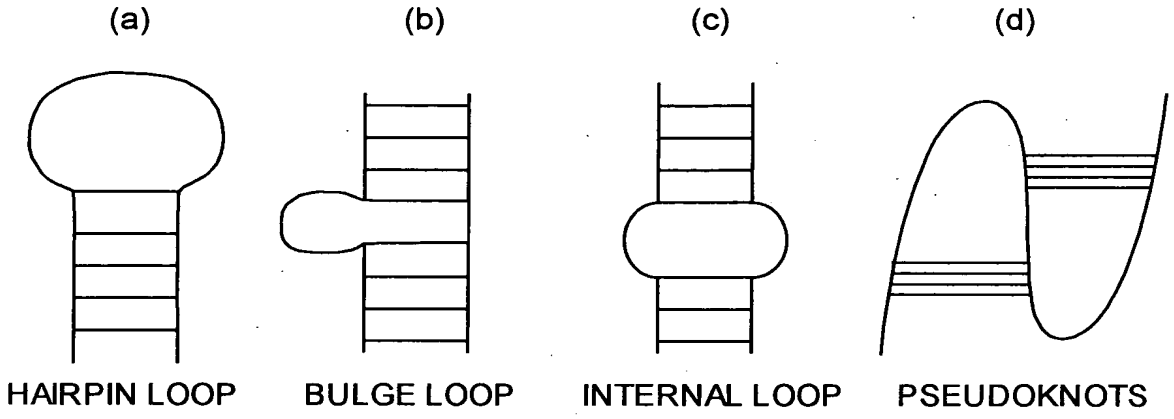
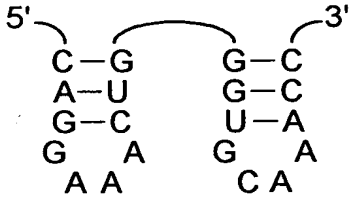


FIG.2

(a) RNA SEQUENCE

C	A	G	G	A	A	A	C	U	G	G	G	U	G	C	A	A	A	C	C

(b) SECONDARY STRUCTURE (STEM STRUCTURE)



(c) PARSE TREE

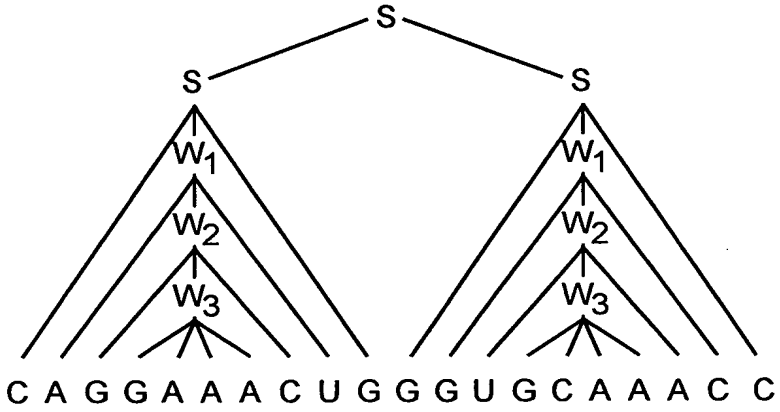


FIG.3

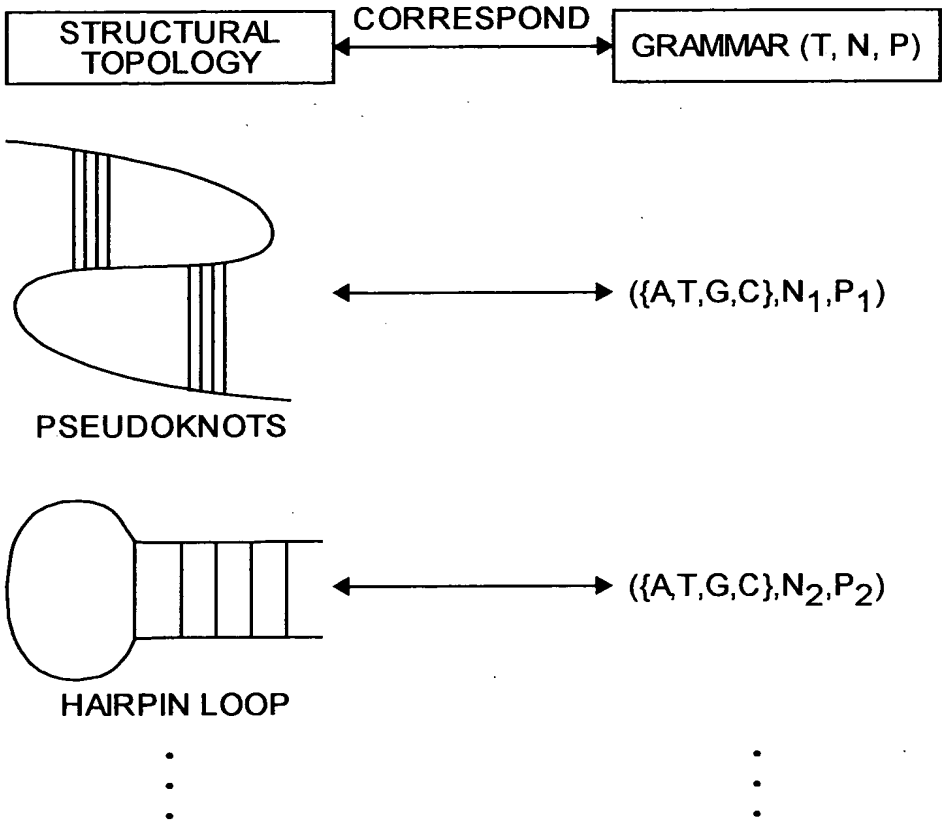

STRUCTURAL TOPOLOGY
CORRESPOND
GRAMMAR (T, N, P)
({A,T,G,C},N1,P1)
PSEUDOKNOTS
({A,T,G,C},N2,P2)
HAIRPIN LOOP

FIG.4

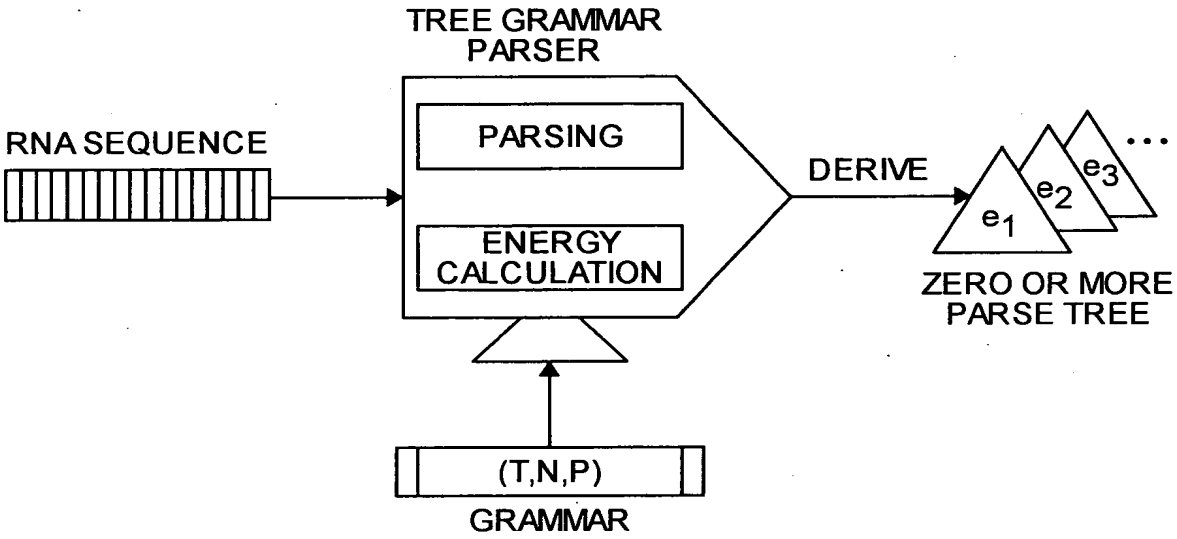

TREE GRAMMAR PARSER
RNA SEQUENCE
PARSING
ENERGY CALCULATION
DERIVE
e1
e2
e3
...
ZERO OR MORE PARSE TREE
(T,N,P)
GRAMMAR

FIG.5

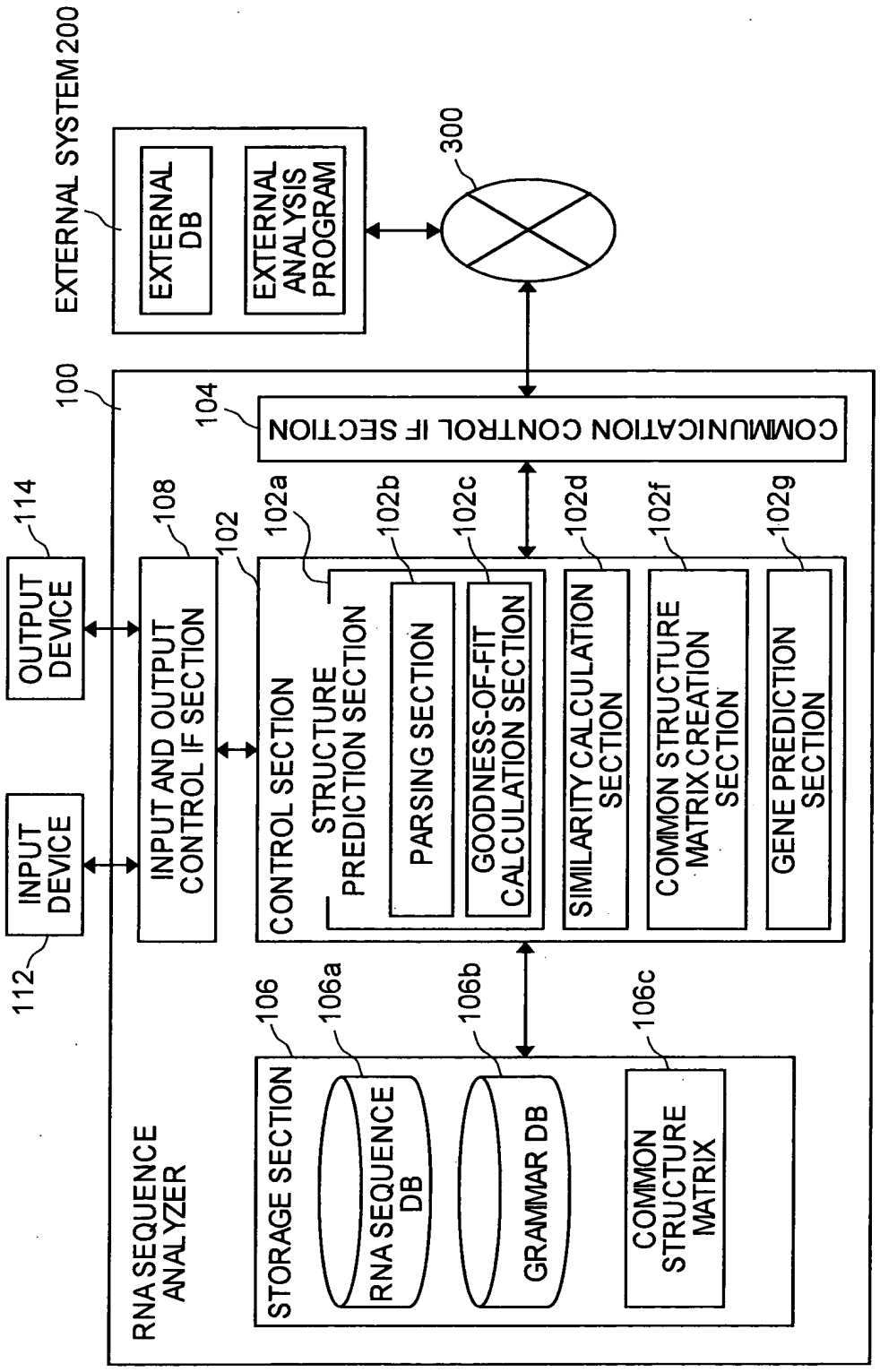

EXTERNAL SYSTEM 200
EXTERNAL DB
EXTERNAL ANALYSIS PROGRAM
300
100
RNA SEQUENCE ANALYZER
104
COMMUNICATION CONTROL IF SECTION
102
CONTROL SECTION
102a
STRUCTURE PREDICTION SECTION
102b
PARSING SECTION
102c
GOODNESS-OF-FIT CALCULATION SECTION
102d
SIMILARITY CALCULATION SECTION
102f
COMMON STRUCTURE MATRIX CREATION SECTION
102g
GENE PREDICTION SECTION
108
INPUT AND OUTPUT CONTROL IF SECTION
114
OUTPUT DEVICE
112
INPUT DEVICE
106
STORAGE SECTION
106a
RNA SEQUENCE DB
106b
GRAMMAR DB
106c
COMMON STRUCTURE MATRIX

FIG.6

GRAMMAR DATABASE 106b

STRUCTURAL TOPOLOGY	GRAMMAR		
	TERMINAL SYMBOL T	NONTERMINAL SYMBOL N	PRODUCTION RULES P
PSEUDOKNOTS	{A,T,G,C}	N_1	P_1
HAIRPIN LOOP		N_2	P_2
INTERNAL LOOP		N_3	P_3
MULTI-BRANCHED LOOP		N_4	P_4
BULGE LOOP		N_5	P_5
⋮		⋮	⋮

FIG.7

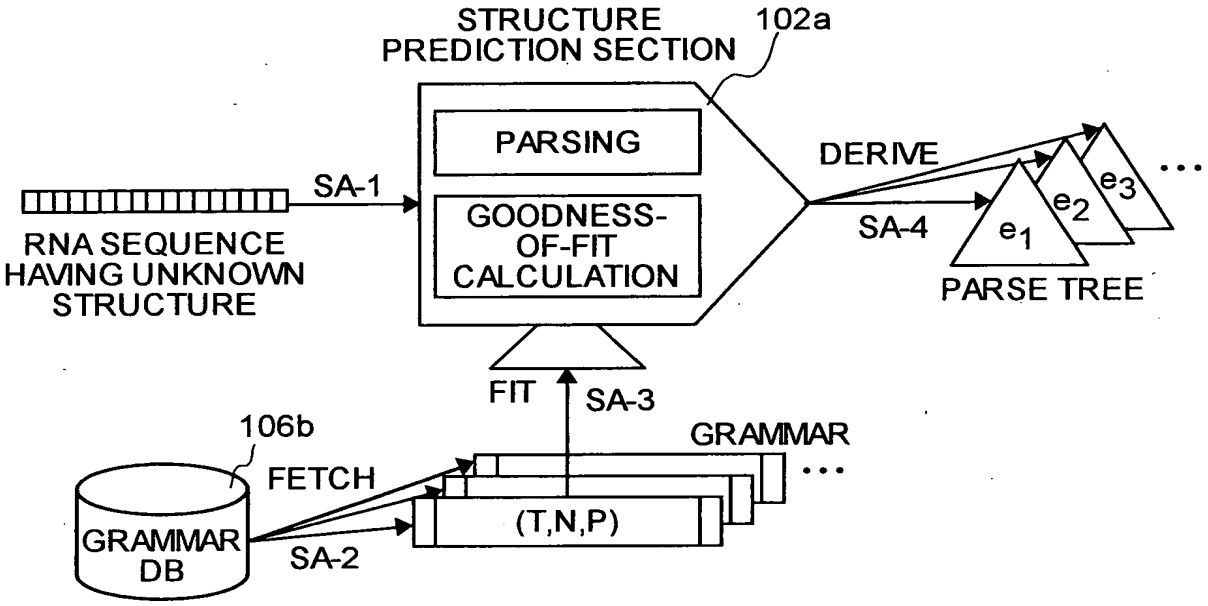

STRUCTURE PREDICTION SECTION
102a
PARSING
GOODNESS-OF-FIT CALCULATION
SA-1
RNA SEQUENCE HAVING UNKNOWN STRUCTURE
DERIVE
SA-4
e1
e2
e3
PARSE TREE
FIT
SA-3
106b
FETCH
GRAMMAR DB
SA-2
GRAMMAR
(T,N,P)

FIG.8

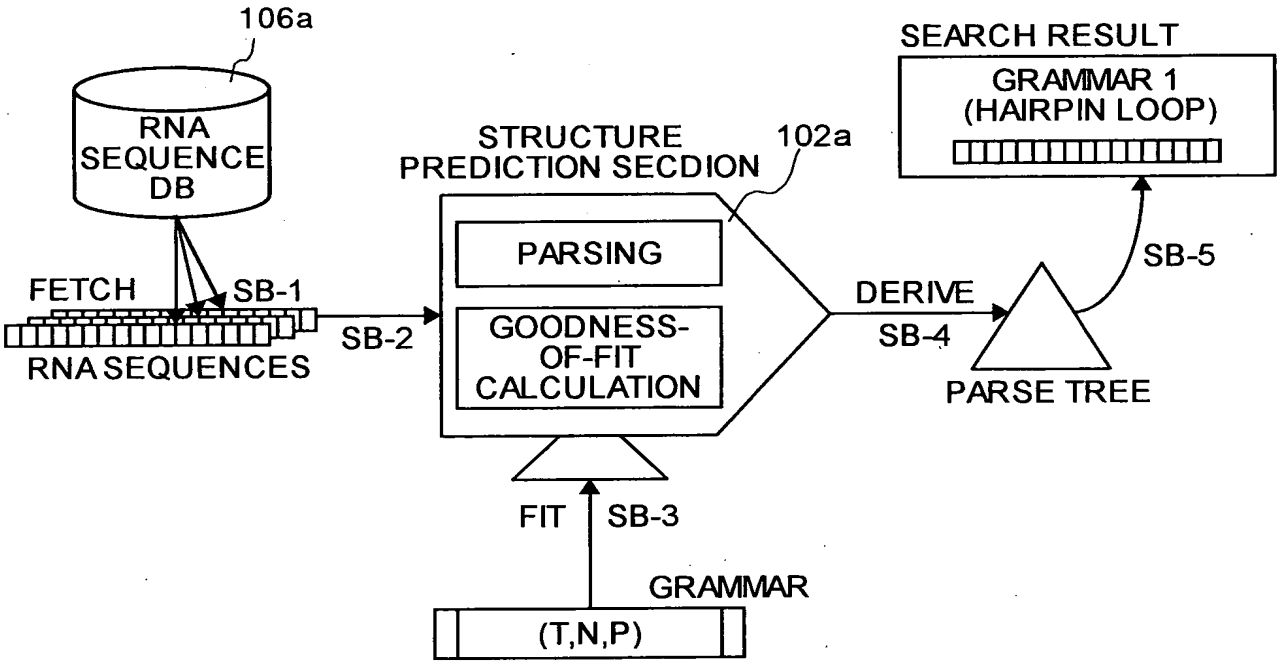

106a
RNA SEQUENCE DB
FETCH
SB-1
RNA SEQUENCES
SB-2
STRUCTURE PREDICTION SECDION
102a
PARSING
GOODNESS-OF-FIT CALCULATION
FIT
SB-3
GRAMMAR
(T,N,P)
DERIVE
SB-4
PARSE TREE
SB-5
SEARCH RESULT
GRAMMAR 1
(HAIRPIN LOOP)

FIG.9

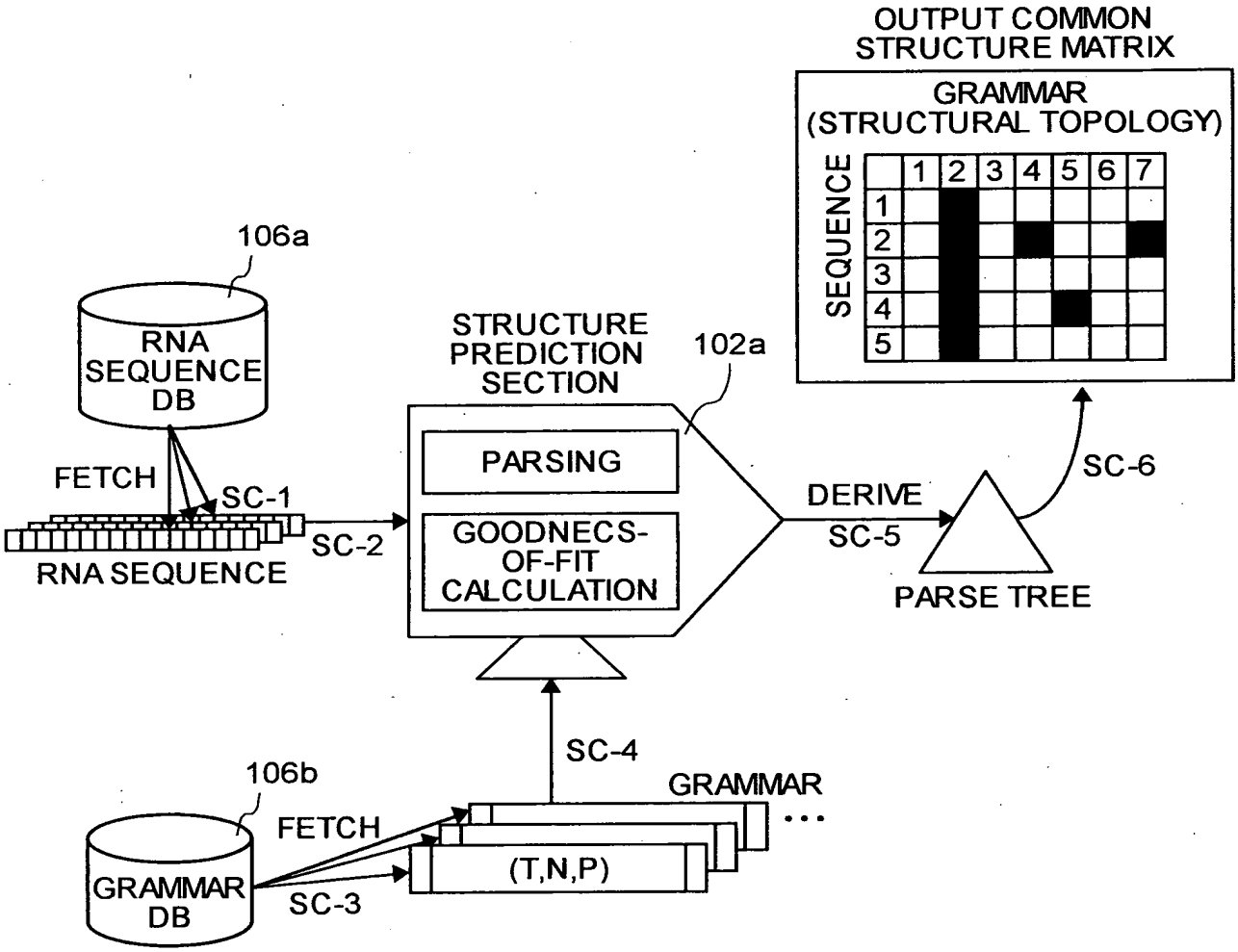

OUTPUT COMMON STRUCTURE MATRIX
GRAMMAR (STRUCTURAL TOPOLOGY)
SEQUENCE
1 2 3 4 5 6 7
106a
RNA SEQUENCE DB
STRUCTURE PREDICTION SECTION
102a
PARSING
GOODNECS-OF-FIT CALCULATION
FETCH
SC-1
SC-2
RNA SEQUENCE
DERIVE
SC-5
SC-6
PARSE TREE
SC-4
106b
GRAMMAR
FETCH
(T,N,P)
GRAMMAR DB
SC-3

FIG.10

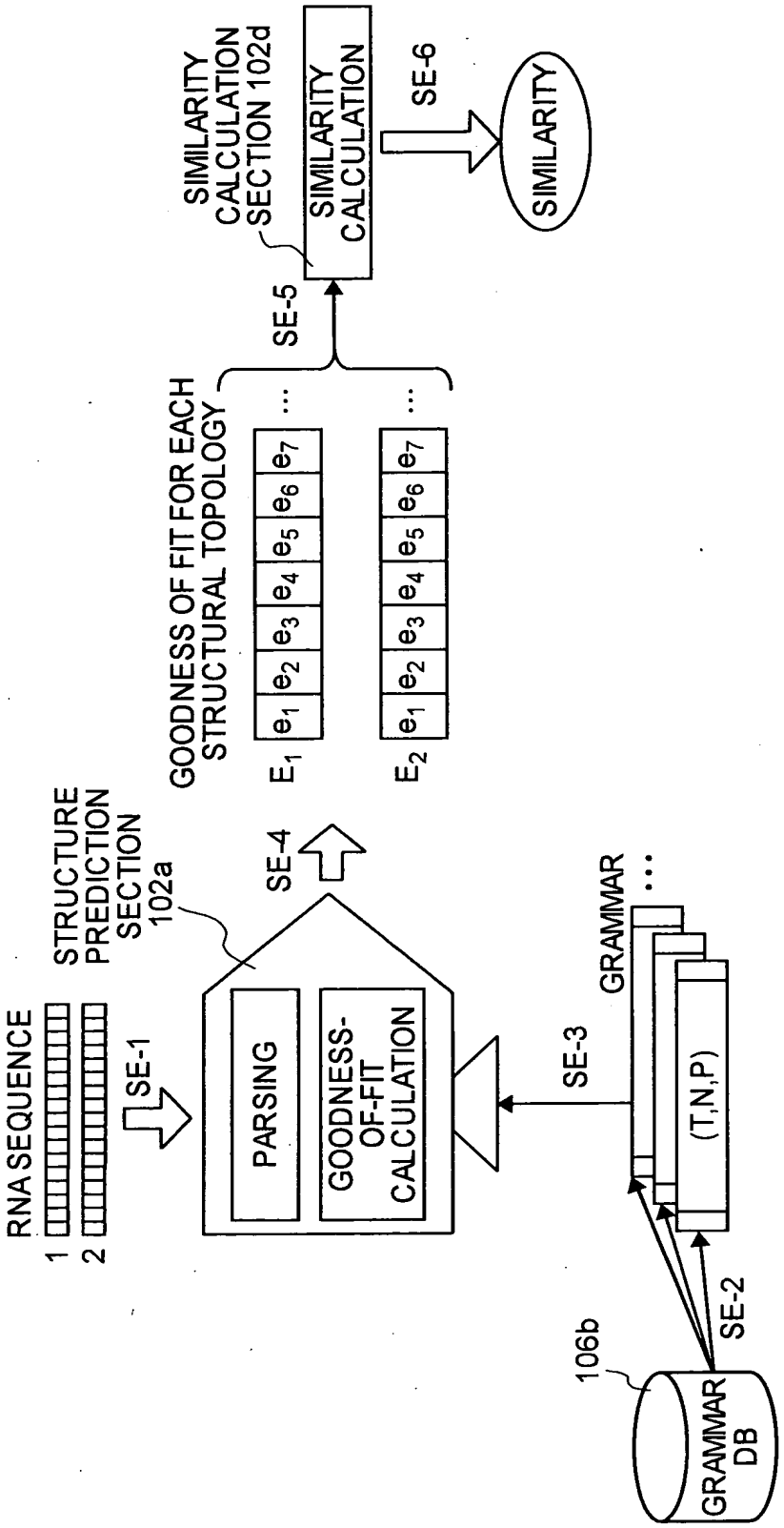

RNA SEQUENCE
1
2
SE-1
STRUCTURE PREDICTION SECTION 102a
PARSING
GOODNESS-OF-FIT CALCULATION
SE-4
GOODNESS OF FIT FOR EACH STRUCTURAL TOPOLOGY
E_1 e_1 e_2 e_3 e_4 e_5 e_6 e_7
E_2 e_1 e_2 e_3 e_4 e_5 e_6 e_7
SE-5
SIMILARITY CALCULATION SECTION 102d
SIMILARITY CALCULATION
SE-6
SIMILARITY
SE-3
GRAMMAR
(T,N,P)
SE-2
106b
GRAMMAR DB

FIG.11

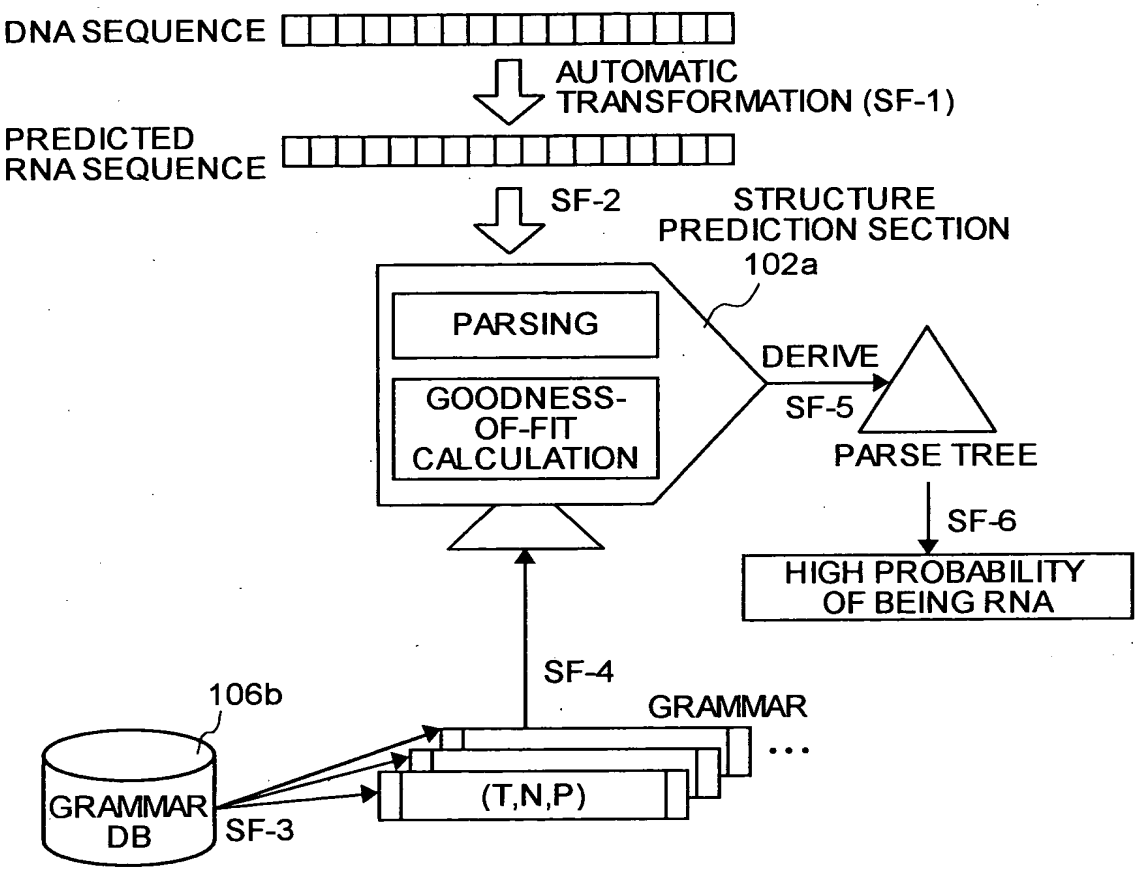

DNA SEQUENCE
AUTOMATIC TRANSFORMATION (SF-1)
PREDICTED RNA SEQUENCE
SF-2
STRUCTURE PREDICTION SECTION
102a
PARSING
GOODNESS-OF-FIT CALCULATION
DERIVE
SF-5
PARSE TREE
SF-6
HIGH PROBABILITY OF BEING RNA
SF-4
106b
GRAMMAR
(T,N,P)
GRAMMAR DB
SF-3

FIG. 12

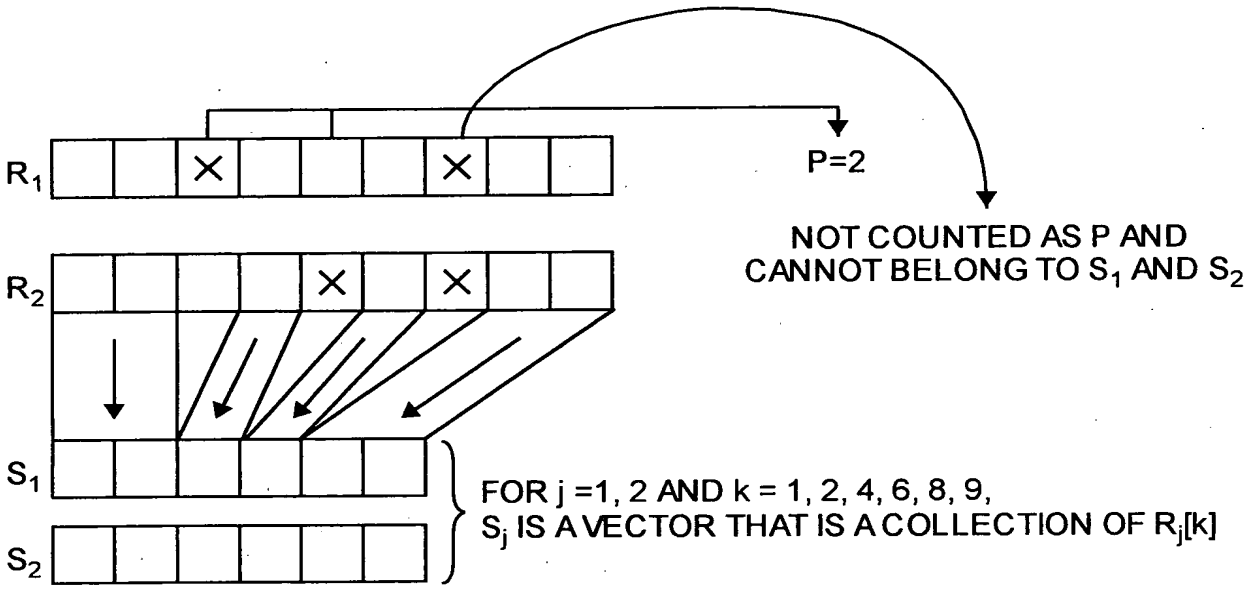

R1
R2
S1
S2
P=2
NOT COUNTED AS P AND CANNOT BELONG TO S1 AND S2
FOR j =1, 2 AND k = 1, 2, 4, 6, 8, 9,
Sj IS A VECTOR THAT IS A COLLECTION OF Rj[k]

FIG.13

(EXAMPLES OF RNA SECONDARY STRUCTURE TOPOLOGY)

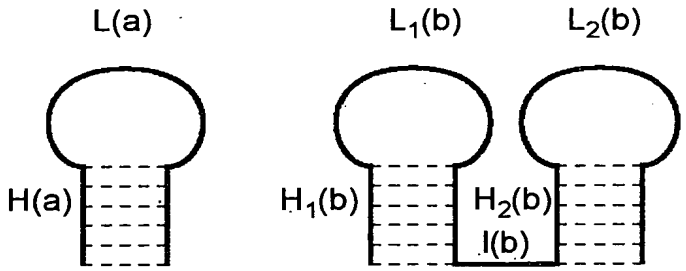


FIG. 14

(PARSE TREES AND SECONDARY STRUCTURES OF S_1)

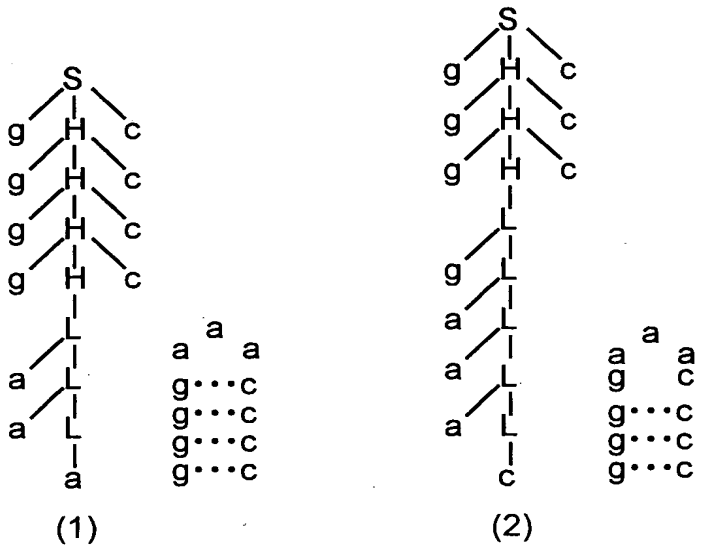


FIG.15

(FREE ENERGIES OF BASE PAIRS [kcal/mol])

3'-SIDE BASE PAIR	5'-SIDE BASE PAIR				
	gu	au	ua	cg	gc
gu	-0.5	-0.5	-0.7	-1.5	-1.3
au	-0.5	-0.9	-1.1	-1.8	-2.3
ua	-0.7	-0.9	-0.9	-1.7	-2.1
cg	-1.9	-2.1	-2.3	-2.9	-3.4
gc	-1.5	-1.7	-1.8	-2.0	-2.9

FIG.16

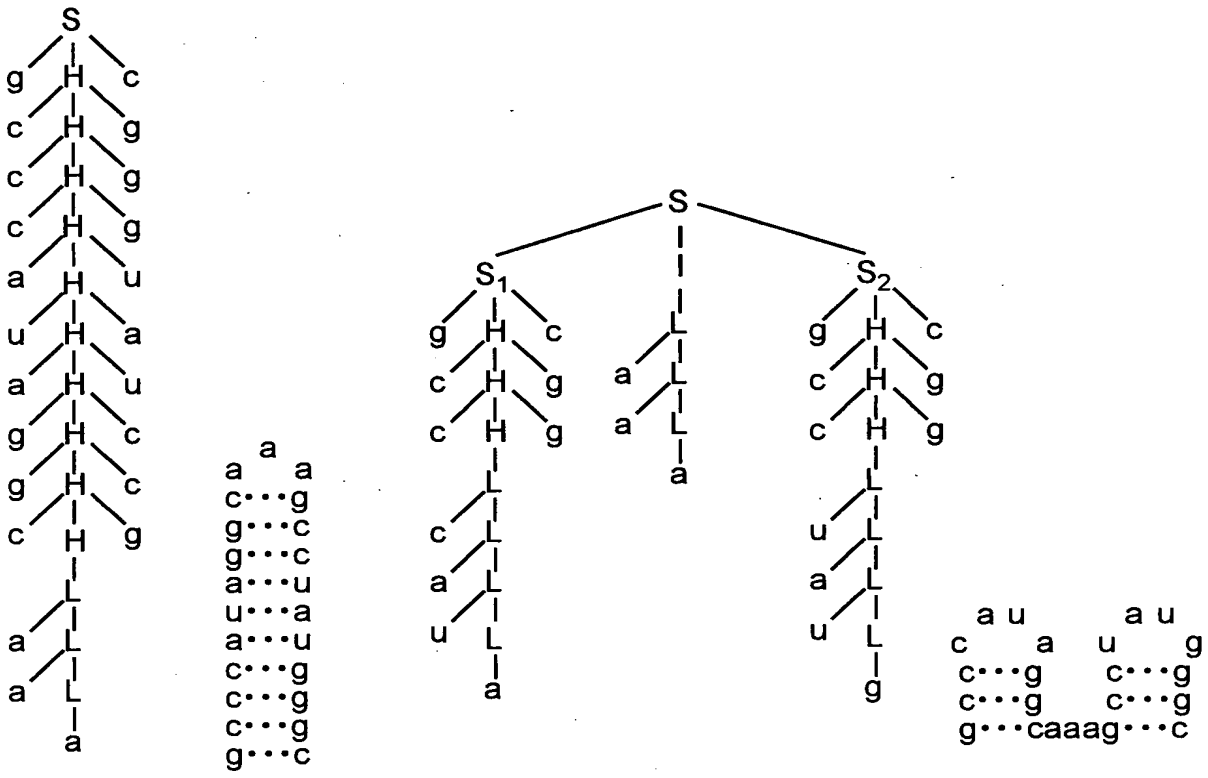
(FREE ENERGIES OF LOOPS [kcal/mol])

LOOP TYPE	LOOP SIZE												
	1	2	3	4	5	6	7	8	9	10	12	14	16
BULGE LOOP	3.3	5.2	6.0	6.7	7.4	8.2	9.1	10.0	10.5	11.0	11.8	12.5	13.0
HAIRPIN LOOP	-	-	7.4	5.9	4.4	4.3	4.1	4.1	4.2	4.3	4.9	5.6	6.1
INTERNAL LOOP	-	0.8	1.3	1.7	2.1	2.5	2.6	2.8	3.1	3.6	4.4	5.1	5.6

Title: RNA SEQUENCE ANALYZER, AND RNA SEQUENCE ANALYSIS METHOD, PROGRAM AND RECORDING MEDIUM
Inventor(s): Yasuo UEMURA et al.
DOCKET NO.: 028567-0133

FIG.17

(OPTIMUM PARSE TREES AND SECONDARY STRUCTURES OF S_2)



(1) DERIVATION BASED ON G_1

(2) DERIVATION BASED ON G_2

FIG.18

RANKING	TOPOLOGY	GOODNESS OF FIT	SECONDARY STRUCTURE
1	STEM LOOP T_1	13.7	SECONDARY STRUCTURE ILLUSTRATED IN Fig. 18(1)
2	DOUBLE-PARALLEL-STEM LOOP T_2	6.7	SECONDARY STRUCTURE ILLUSTRATED IN Fig. 18(2)

FIG.19

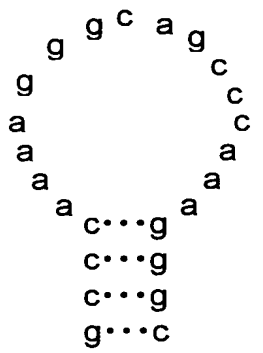
SEQUENCE	GOODNESS OF FIT	SECONDARY STRUCTURE
s_2	6.7	SECONDARY STRUCTURE ILLUSTRATED IN Fig. 18(2)

FIG.20

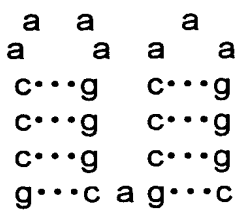
	T_1	T_2
s_1	1.4	-
s_2	13.6	6.7

FIG.21

(OPTIMUM SECONDARY STRUCTURE OF s)



(1)



(2)

FIG.22

	T_1	T_2
s	-	5.1

FIG.23

SEQUENCE	GOODNESS OF FIT	TOPOLOGY (SCORE)
S_2	6.7	$T_2(5.1)$